

Replace the first paragraph on pag 12 with:

C2
Fig. 8A depict the amino acid sequences of type 1 pilus subunits (FimA (Seq. ID No: 62), FimF (Seq. ID No: 63), FimG (Seq. ID No: 64), FimH (Seq. ID No: 65)). The end of the mannose binding lectin domain and the start of the pilin domain in FimH are indicated by vertical arrows above the sequences. Type 1 pilin subunits (FimA, FimF, FimG) were aligned with the pilin domain of FimH using Clustal W and manually adjusted to minimize gaps in secondary structure elements. Gaps in the alignment are indicated by dots. Sequence numbering for FimH starts at position 22 in the pre-protein. Residues involved in chaperone binding are indicated by an open circle above the residue. Residues in the carbohydrate binding pocket are boxed. A large box marks the NH₂-terminal extensions in the pilin subunits. The conserved b-zipper motif found in all pilin subunits corresponds to the F beta-strand. Limits and nomenclature for secondary structure elements are shown below the sequence.

IN THE CLAIMS

Please add new claim 136.

C3
136. (new) The compound of claim 1 wherein the compound consists of SEQ ID NO:12.